



#4

SEQUENCE LISTING

<110> Tse Wei-chang
Liming Yu

<120> Hybrid with Interferon-alpha and an
Immunoglobulin Fc for Treatment of Tumors

<130> 95-2AAA

<140> 09/268,787

<141> 1999-03-16

<150> 08/994,719

<151> 1997-12-19

<150> 08/719,331

<151> 1996-09-25

<150> 08/579,211

<151> 1995-12-28

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (1251)

<223> recombinant sequence based on human sequences

<400> 1

atg	gcc	ttg	acc	ttt	gtt	tta	ctg	gtg	gcc	ctc	ctg	gtg	ctc	agc	tgc
Met															Cys
1															15

48

aag	tca	agc	tgc	tct	ctg	ggc	tgt	gat	ctg	cct	caa	acc	cac	agc	ctg
Lys	Ser	Ser	Cys	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu
20															30

96

ggt	agc	agg	agg	acc	ttg	atg	ctc	ctg	gca	cag	atg	agg	aaa	atc	tct
Gly	Ser	Arg	Arg	Thr	Leu	Met	Leu	Leu	Ala	Gln	Met	Arg	Lys	Ile	Ser
35															45

144

ctt	ttc	tcc	tgc	ttg	aag	gac	aga	cat	gac	ttt	gga	ttt	ccc	cag	gag
Leu	Phe	Ser	Cys	Leu	Lys	Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glut
50															60

192

gag ttt ggc aac cag ttc caa aag gct gaa acc atc cct gtc ctc cat Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His	240
65 70 75 80	
gag atg atc cag cag atc ttc aat ctc ttc agc aca aag gac tca tct Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser	288
85 90 95	
gct gct tgg gag acc ctc cta gac aaa ttc tac act gaa ctc tac Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr	336
100 105 110	
cag cag ctg aat gac ctg gaa gcc tgg atg cag ggg gtg ggg gtg Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val	384
115 120 125	
aca gag act ccc ctg atg aag gag gac tcc att ctg gct gtg agg aaa Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys	432
130 135 140	
tac ttc caa aga atc act ctc tat ctg aaa gag aag aaa tac agc cct Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro	480
145 150 155 160	
tgt gcc tgg gag gtt gtc aga gca gaa att atg aga tct ttt tct ttg Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu	528
165 170 175	
tca aca aac ttg caa gaa agt tta aga agt aag gaa gag tcc aaa tat Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Glu Ser Lys Tyr	576
180 185 190	
ggt ccc ccg tgc cca tca tgc cca gca cct gag ttc ctg ggg gga cca Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro	624
195 200 205	
tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg atc tcc Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser	672
210 215 220	
cgg acc cct gag gtc acg tgc gtg gtg gac gtg agc cag gaa gac Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp	720
225 230 235 240	
ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg cat aat Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn	768
245 250 255	
gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac cgt gtg Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val	816
260 265 270	
gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc aag gag Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu	864

275	280	285	
tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc gag aaa Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys 290	295	300	912
acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg tac acc Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 305	310	315	960
ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc ctg acc Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr 325	330	335	1008
tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 340	345	350	1056
agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 355	360	365	1104
gac tcc gac ggc tcc ttc ctc tac agc agg ctg acc gtg gac aag Asp Ser Asp Gly Ser Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys 370	375	380	1152
agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu 385	390	395	1200
gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct ctg ggt Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly 405	410	415	1248
aaa tag Lys			1254

<210> 2
<211> 417
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial peptide sequence based on human
sequence

<400> 2
Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
1 5 10 15
Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30
Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser
35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
 50 55 60
 Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
 65 70 75 80
 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
 85 90 95
 Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110
 Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
 130 135 140
 Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160
 Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175
 Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Glu Ser Lys Tyr
 180 185 190
 Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 195 200 205
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 210 215 220
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 225 230 235 240
 Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 245 250 255
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
 260 265 270
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 275 280 285
 Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
 290 295 300
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 305 310 315 320
 Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 325 330 335
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 340 345 350
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 355 360 365
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
 370 375 380
 Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 385 390 395 400
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 405 410 415
 Lys

<210> 3
 <211> 2
 <212> PRT
 <213> Artificial Sequence

<220>

<223> artificial peptide linker sequence

<400> 3

Gly Ser

1

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial peptide linker sequence

<400> 4

Gly Gly Ser Gly Gly Gly Ser

1

5

<210> 5

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial peptide linker sequence

<400> 5

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

<210> 6

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial peptide linker sequence

<400> 6

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly

1

5

10

15

Ser

<210> 7

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial peptide linker sequence

<400> 7

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly

1

5

10

15

Gly Ser Gly Gly Gly Gly Ser
20

<210> 8
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial peptide linker sequence

<400> 8
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
20 25 30

<210> 9
<211> 40
<212> PRT
<213> artificial sequence

<220>
<223> artificial peptide linker sequence

<400> 9
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
20 25 30
Gly Gly Ser Gly Gly Gly Ser
35 40

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial peptide linker sequence

<400> 10
Gly Gly Ser Gly Gly Ser
1 5

<210> 11
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> artificial peptide linker sequence

<400> 11
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser

1

5

10

15